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☐ 1: [U95825](#)[gi:4539617] This record was replaced or removed. See [revision history](#) for details.

LOCUS HSU95825 4392 bp mRNA linear PRI 30-MAR-1999
 DEFINITION Human androgen-induced prostate proliferative shutoff associated
 protein (AS3) mRNA, complete cds.
 ACCESSION U95825
 VERSION U95825.1 GI:4539617
 KEYWORDS .
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 4392)
 AUTHORS Geck,P., Szelei,J., Jimenez,J., Soto,A.M. and Sonnenschein,C.
 TITLE Androgen-induced proliferative shutoff in prostate cancer cells
 JOURNAL Proc. Annu. Meet. Am. Assoc. Cancer Res. 37, 223-223 (1996)
 REFERENCE 2 (bases 1 to 4392)
 AUTHORS Geck,P., Szelei,J., Jimenez,J., Sonnenschein,C. and Soto,A.M.
 TITLE Early gene expression during androgen-induced inhibition of
 proliferation of prostate cancer cells: a new suppressor candidate
 on chromosome 13, in the BRCA2-Rb1 locus
 JOURNAL J. Steroid Biochem. Mol. Biol. 68, 41-45 (1999)
 REFERENCE 3 (bases 1 to 4392)
 AUTHORS Geck,P., Szelei,J., Jimenez,J., Sonnenschein,C. and Soto,A.M.
 TITLE Direct Submission
 JOURNAL Submitted (28-MAR-1997) Anatomy and Cell Biology, Tufts University
 Medical School, 136 Harrison Avenue, Boston, MA 02111, USA
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Sep 16 2003 13:15:10



Sequence Revision History

PubMed

Nucleotide

Protein

Genome

Structure

PMC

Taxonomy

OMIM

Find (Accessions, GI numbers or Fasta style SeqIds) 

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Entrez

Gi	Version	Update Date
4559409	2	Apr 5 1999 1:29
4539617	1	Mar 30 1999 12:03

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LocusLink provides curated information for human, fruit fly, mouse, rat, and zebrafish

LOCUS HSU95825 5253 bp mRNA linear PRJ
 LOCUS HSU95825 4392 bp mRNA linear PRJ
 DEFINITION Human androgen-induced prostate proliferative shutoff protein (AS3) mRNA, complete cds.

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ACCESSION U95825
 VERSION U95825.2 GI:4559409
 VERSION U95825.1 GI:4539617

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KEYWORDS .
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eumammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Check sequence revision history

REFERENCE 1 (bases 1 to 4392)

How to create WWW links to Entrez

AUTHORS Geck, P., Szelei, J., Jimenez, J., Soto, A.M. and Sonnenschein, C.
 TITLE Androgen-induced proliferative shutoff in prostate cancer cells
 JOURNAL Proc. Annu. Meet. Am. Assoc. Cancer Res. 37, 223-223 (1996)

LinkOut

REFERENCE 2 (bases 1 to 5253)
 REFERENCE 2 (bases 1 to 4392)

Cubby

AUTHORS Geck, P., Szelei, J., Jimenez, J., Sonnenschein, C. and Soto, A.M.
 TITLE Early gene expression during androgen-induced inhibition of proliferation of prostate cancer cells: a new suppressor gene on chromosome 13, in the BRCA2-Rb1 locus
 JOURNAL J. Steroid Biochem. Mol. Biol. 68 (1-2), 41-50 (1999)

Related resources

MEDLINE 99229875
 PUBMED 10215036

BLAST

REFERENCE 3 (bases 1 to 5253)
 JOURNAL J. Steroid Biochem. Mol. Biol. 68, 41-45 (1999)
 REFERENCE 3 (bases 1 to 4392)

Reference sequence project

AUTHORS Geck, P., Szelei, J., Jimenez, J., Sonnenschein, C. and Soto, A.M.
 TITLE Direct Submission

LocusLink

JOURNAL Submitted (28-MAR-1997) Anatomy and Cell Biology, Tufts Medical School, 136 Harrison Avenue, Boston, MA 02111,

Clusters of orthologous groups

REFERENCE 4 (bases 1 to 5253)
 AUTHORS Geck, P., Szelei, J., Jimenez, J., Sonnenschein, C. and Soto, A.M.
 TITLE Direct Submission

Protein reviews on the web

JOURNAL Submitted (05-APR-1999) Anatomy and Cell Biology, Tufts Medical School, 136 Harrison Avenue, Boston, MA 02111,
 REMARK Sequence update by submitter

COMMENT On Apr 5, 1999 this sequence version replaced gi:4539617
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FEATURES Location/Qualifiers

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661 ccattgtctc atgaaccatc ctgatttagc aaaagactta acagagtatc tt
721 gtcacatgac cctgaggaag ctattagaca tgatgttatt gtgtcaatag tt

```



```

781 taaaaaggat attcttctgg tcaatgatca cttacttaat tttgtgagag ag
841 agacaaacga tggagagtag gcaaagaagc catgatggga cttgccccaa tt
901 atatgcttta cagtcagcag ctggaaaaga tgctgcaaaa cagatagcat gg
961 caaattgcta catatatatt atcaaaatag tattgatgat cgactacttg tt
1021 ctttgtctca tacatggttc ctcaaatctt agaaactaca gaacggatga aa
1081 ttacttgtat gccacactgg atttaaagtc tgtgaaagca ttgaatgaaa tg
1141 tcaaaatctg ctccgacatc aagtaaagga tttgcttgac ttgattaagc aa
1201 agatgccagt gtcaaggcca ttttttcaaa agtgatgggt attacaagaa at
1261 tcctggtaag gctcaggatt tcatgaagaa attcacacag gtggttagaag at
1321 aataagaaag cagttagaag tacttgtagg tccaacatgc tcctgcaagc ag
1381 ttgtgtgcgt gaaataacta agaagttggg caacccccaa cagcctacaa at
1441 ggaaatgatc aagtttctct tggagaggat agcacctgtg cacatagata cc
1501 cagtgtctct attaaacaag tgaacaaatc aatagatgga acagcagatg at
1561 ggggtgtcca actgatcaag ccatcagagc aggtcttgaa ctgcttaagg ta
1621 tacacatccc atctcatttc attctgctga aacatttgaa tcattactgg ct
1681 aatggatgat gaaaaagtag cagaagctgc actacaaatt ttcaaaaaca ca
1741 aattgaagag gatthttccac acatcagatc agccttgctt cctgttttac at
1801 taaaaaagga ccccccgctc aagccaaata tgccattcat tgtatccatg cc
1861 tagtaaagag acccagtttg cacagatatt tgagcctctg cataagagcc ta
1921 caacctggaa catctcataa caccattggg tactattggg catattgctc tc
1981 tgatcaattt gctgctcctt ggaaatcctg ggtagctact ttcatgtgta aa
2041 catgaatgat cggcttccag ggaaaaagac aactaaactt tgggttccag at
2101 atctcctgag acaatgggca aaattcaggc tattaaaatg atgggttcgag gg
2161 aatgaaaaat aatcacagta aatcaggaac ttctacctta agattgctaa ca
2221 gcatagtgat ggagacttga cagaacaggg gaaaattagt aaaccagata tg
2281 gagacttgct gctgggagtg ctatttgtaa gctggcaca gaacctgtt ac
2341 catcacatta gaacaatata agctatgtgc attagctatc aacgatgaat gc
2401 aagacaagtg tttgccaga aacttcacaa aggcctttcc cgtttacggc tt
2461 gtatatggca atctgtgccc tttgtgcaaa agatcctgta aaggagagaa ga
2521 taggcaatgt ttggtgaaaa atataaatgt aaggcgggag tatctgaagc ag
2581 tgttagtgaa aaattattgt ctcttctacc agagtatgtt gttccatata ca
2641 tttggcacat gaccagatt atgtcaaagt acaggatatt gaacaactta aa
2701 agaatgtctt tggtttggtc tggaaatatt aatggctaaa aatgaaaata ac
2761 ttttatcaga aagatggtag aaaatatata acaaacaaaa gatgcccaag ga
2821 tgcaaaaatg aatgaaaaac tgtacactgt gtgtgatgtt gccatgaata tc
2881 aaagagtact acatacagtt tggaaatctc taaagaccog gtactaccag ct
2941 cactcaacct gacaagaatt tcagtaacac caaaaattat ctgcctcctg aa
3001 atttttctact cctggaaaac ctaaaacaac caatgttcta ggagctgtta ac
3061 ttcacagca ggcaagcaat ctgagccaa atcatcacga atggaaactg ta
3121 aagcagcagc tcaaatccaa gctctcctgg aagaataaag gggaggcttg at
3181 aatggatcac agtgaaaatg aagattacac aatgtcttca cctttgcccgg gg
3241 tgacaagaga gacgactctg atcttgtaag gtctgaattg gagaagccta ga
3301 aaaaacgccc gtcacagaac agggaggagaa attaggtatg gatgacttga ct
3361 acaggaacag aaacctaaag gcagtcagcg aagtcggaaa agaggccata cc
3421 atctgatgaa cagcagtggc ctgaggaaaa gaggtcaaaa gaagatatat ta
3481 agatgaacag aatagtccgc caaaaaaggg taaaagaggc cgaccacca aa
3541 tggaggtaca ccaaaagaag agccaacaat gaaaacttct aaaaaaggaa gc
3601 atctggacct ccagcaccag agggaggagga agaagaagaa agacaaagtg ga
3661 acagaagtcc aaaagcaaac agcaccgagt gtcaaggaga gcacagcaga ga
3721 tcctgaatct agtgcaattg aatccacaca gtccacacca cagaaaggac ga
3781 atcaaaaacg ccatcaccat cacaacccaa aaaaaatgtg taagttgtaa at
3841 tcaaaccaat ttcaaattat tttgcaaaaag ttcttaaatt tgtaaacata ca
3901 tatthaaatt ccatatattt agccccatta cactaggtac ggcggcgaag tg
3961 gaacggcgat gaacaaatgt aattaataac tttctctgtg aaagcttttg aa
4021 tttttttttt tttttttttg gtcaagcttg aggtgaata aagcctttga tg
4081 gggactgctg aagagtggac agttggacct tactttgggtg accccatata tt
4141 catgctttag ccatacacat ggtaacattg actatggagt cttgtgaaag tg
4201 gatggctatg tagacataaa gaagaaactt gtaaatatct ttttcttttt tt
4261 tctgatttct gaagtgtctg tatagctttt atctgcccgt ttaaactgac ag
4321 tgtttatttg atctattgat ttgaaaagaa tttgttagga tagatcttaa gc

```

4381 gtcagtgttt gt
//

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[NCBI](#) | [NLM](#) | [NIH](#)



Sequence Revision History

PubMed

Nucleotide

Protein

Genome

Structure

PMC

Taxonomy

OMIM

Find (Accessions, GI numbers or Fasta style Seqlds) 

About Entrez

Show difference in format

Entrez

Gi	Version	Update Date
4559409	2	Apr 5 1999 1:29
4539617	1	Mar 30 1999 12:03

Search for Genes

LocusLink provides curated information for human, fruit fly, mouse, rat, and zebrafish

Number of accessions to be compared: Old = 1, New = 1

Number of matched accessions: 1

Number of unmatched accessions: Old = 0, New = 0

Help|FAQ

Accession = U95825, Locus = HSU95825

=====

Batch Entrez: Upload a file of GI or accession numbers to retrieve proteins or nucleotide sequences

Differences in LOCUS names:

old: "LOCUS	HSU95825	4392 bp	mRNA	linear
-------------	----------	---------	------	--------

Check sequence revision history

	30-MAR-1999"			
new: "LOCUS	HSU95825	5253 bp	mRNA	linear

05-APR-1999"

How to create WWW links to Entrez

Differences in VERSION:

LinkOut

old: "U95825.1 GI:4539617"

Cubby

new: "U95825.2 GI:4559409"

Differences in BASECOUNT:

Related resources

old: " 1508 a 801 c 894 g 1189 t"

BLAST

new: " 1755 a 944 c 1074 g 1480 t"

Reference sequence project

Differences in COMMENT:

LocusLink

old: "[WARNING] On Apr 5, 1999 this sequence was replaced by a new

Clusters of orthologous groups

gi:4559409."

new: "On Apr 5, 1999 this sequence version replaced gi:4539617."

Protein reviews on the web

Differences in SEQUENCE:

First base with diff: 1
 The number of diffs: 3245
 Old length: 4392
 New length: 5253

Threshold: 10

Bases with diffs: 1, 2, 3, 4, 6, 8, 9, 10, 11

Differences in FEATURE.source:

```
-----
Old feature      source      1..4392
                  /note              = "exons 1-21 map to cosmid 267p19;
                               22-31 map to cosmid PAC49J10"
                  /organism           = "Homo sapiens"
                  /mol_type            = "mRNA"
                  /db_xref              = "taxon:9606"
                  /chromosome          = "13"
                  /map                  = "13q12-q13"
                  /cell_line            = "LNCaP"
                  /cell_type            = "cancer cells"
                  /tissue_type          = "prostate"
```

Differences in FEATURE.gene:

```
-----
Old feature      gene        1..4392
                  /gene              = "AS3"
```

Differences in FEATURE.exon:

```
-----
Old feature      exon        47..144
                  /gene              = "AS3"
                  /number            = "2"
```

Differences in FEATURE.exon:

```
-----
Old feature      exon        145..271
                  /gene              = "AS3"
                  /number            = "3"
```

Differences in FEATURE.CDS:

```
-----
Old feature      CDS          170..3823
                  /gene              = "AS3"
                  /codon_start        = "1"
                  /product              = "androgen-induced prostate prolifer-
                               shutoff associated protein"
                  /protein_id          = "AAD22134.1"
                  /db_xref              = "GI:4539618"
                  /translation          = "MHMV DLMSSII CEGDTVSQELLDTVLVNLVPA
AKALLKRTAQAI EPYITTFNQV LMLGKTSIS
ELYNIDSHLLLSVLPQLEFKLSNDNEERLQV
DSELASQNKPLWQCYLGRFNDIHVPIRLECVI
LAKDLTEYLKVRSHDPEEAI RHDVIVSIVTAI
LNFVRERTLDKRWRVRKEAMMGLAQIYKKYAI
IAWIKDKLLHIYYQNSIDRLLVERIFAQYMI
CLYYLYATLDLNAV KALNEMWKCQNLLRHQVI
DASVKAIFSKVMVITRNLPDPGKAQDFMCKKF
QLEVLVSPTCSCQAEGCVREITKKLG NPKQI
LERIAPVHIDTESISALIKQVNKSIDGTADDI
AGLELLKVLSFTHPI SFHSAETFESLLACLK
IFKNTGSKIEEDFP HIRSALLPVLHHSKKG
HAIFSSKETQFAQIF EPLHKS LDP SNLEHLIT
APDQFAAPWKS WVATFIVKDLLMNDRLPGKKI
PETMVKIQA IKMMVRWLLGMKNH SKSGTSTI
DLTEQGKISKPDMSRLRLAAGSAIVKLAQEP"
```

LCALAINDECYQVRQVFAQKLHKGLSRLRLPI
 DPKERRAHARQCLVKININVRREYLKQHAAVS
 VPYTIHLLAHDPDYVKVQDIEQLKDVKECLWI
 NSHAFIRKMVENIKQTKDAQGPDDAKMNEKL)
 SKSTTYSLESPKDPVLPARFFTQPDKNFSNTI
 TPGKPKTTNVLGAVNKPLSSAGKQSQTSSRI
 PSSPGRIKGRLDSEMDHSENYDTMSSPLPC
 VRSELEKPRGRKKTPTVTEQEEKLGMDDLTKLA
 RKRGHASESEDEQQWPPEEKRLKEDIENEDEQ
 PPKPLGGGTPKEEPTMKTSKKGSKKSGPPAI
 NTEQSKSKQHRVSRRAQRAESPESAIEST
 SKTPSPSQPKQNV"

Differences in FEATURE.exon:

 Old feature exon 272..352
 /gene = "AS3"
 /number = "4"

Differences in FEATURE.exon:

 Old feature exon 353..493
 /gene = "AS3"
 /number = "5"

Differences in FEATURE.exon:

 Old feature exon 494..609
 /gene = "AS3"
 /number = "6"

Differences in FEATURE.exon:

 Old feature exon 610..704
 /gene = "AS3"
 /number = "7"

Differences in FEATURE.exon:

 Old feature exon 705..850
 /gene = "AS3"
 /number = "8"

Differences in FEATURE.exon:

 Old feature exon 851..1002
 /gene = "AS3"
 /number = "9"

Differences in FEATURE.exon:

 Old feature exon 1003..1116
 /gene = "AS3"
 /number = "10"

Differences in FEATURE.exon:

 Old feature exon 1117..1198
 /gene = "AS3"
 /number = "11"

Differences in FEATURE.exon:

Old feature exon 1199..1247
 /gene = "AS3"
 /number = "12"

Differences in FEATURE.exon:

Old feature exon 1248..1387
 /gene = "AS3"
 /number = "13"

Differences in FEATURE.exon:

Old feature exon 1388..1503
 /gene = "AS3"
 /number = "14"

Differences in FEATURE.exon:

Old feature exon 1504..1609
 /gene = "AS3"
 /number = "15"

Differences in FEATURE.exon:

Old feature exon 1610..1770
 /gene = "AS3"
 /number = "16"

Differences in FEATURE.exon:

Old feature exon 1771..1894
 /gene = "AS3"
 /number = "17"

Differences in FEATURE.exon:

Old feature exon 1895..2053
 /gene = "AS3"
 /number = "18"

Differences in FEATURE.exon:

Old feature exon 2054..2122
 /gene = "AS3"
 /number = "19"

Differences in FEATURE.exon:

Old feature exon 2123..2259
 /gene = "AS3"
 /number = "20"

Differences in FEATURE.exon:

Old feature exon 2260..2383
 /gene = "AS3"
 /number = "21"

Differences in FEATURE.exon:

Old feature exon 2384..2588
 /gene = "AS3"
 /number = "22"

Differences in FEATURE.exon:

Old feature exon 2589..2703
 /gene = "AS3"
 /number = "23"

Differences in FEATURE.exon:

Old feature exon 2704..2836
 /gene = "AS3"
 /number = "24"

Differences in FEATURE.exon:

Old feature exon 2837..2956
 /gene = "AS3"
 /number = "25"

Differences in FEATURE.exon:

Old feature exon 2957..3019
 /gene = "AS3"
 /number = "26"

Differences in FEATURE.exon:

Old feature exon 3020..3165
 /gene = "AS3"
 /number = "27"

Differences in FEATURE.exon:

Old feature exon 3166..3271
 /gene = "AS3"
 /number = "28"

Differences in FEATURE.exon:

Old feature exon 3272..3711
 /gene = "AS3"
 /number = "29"

Differences in FEATURE.exon:

Old feature exon 3712..3936
 /gene = "AS3"
 /number = "30"

Differences in FEATURE.exon:

Old feature exon 3937..4392
 /gene = "AS3"
 /number = "31"

Differences in FEATURE.source:

```

-----
New feature      source      1..5253
                  /note              = "exon 1 maps to P1 Artificial Chr
                                PAC26H23; exons 2-24 map to cosm
                                exons 25-34 map to P1 Artificial
                                Chromosome PAC 49J10"
                  /organism          = "Homo sapiens"
                  /mol_type          = "mRNA"
                  /db_xref           = "taxon:9606"
                  /chromosome        = "13"
                  /map               = "13q12-q13"
                  /cell_line         = "LNCaP"
                  /cell_type         = "cancer cells"
                  /tissue_type       = "prostate"

```

Differences in FEATURE.gene:

```

-----
New feature      gene      1..5253
                  /gene              = "AS3"

```

Differences in FEATURE.exon:

```

-----
New feature      exon      47..173
                  /gene              = "AS3"
                  /number            = "2"

```

Differences in FEATURE.CDS:

```

-----
New feature      CDS      66..4241
                  /gene              = "AS3"
                  /codon_start       = "1"
                  /product            = "androgen-induced prostate proli
                                shutoff associated protein"
                  /protein_id         = "AAD22134.2"
                  /db_xref           = "GI:4559410"
                  /translation        = "MAHSKTRTNDGKITYPGPKVEISDKISKEEM
                                DMDQDSEEEKELYLNLAHLASDFFLKHPDKI
                                IFRIYAPEAPYTSPPDKLKDIFMFITRQLKGLF
                                YLLENIAWVKSYNICEFELEDSNEIFTQLYRTI
                                VHMHMVDLMSSIIICGDTVVSQELLDTVLVNLA
                                DLAKALLKRTAQAIPEYITNFFNQVLMGKTS
                                ILELYNIDSHLLLSVLPQLEFKLKSNDNEERI
                                AKDSELASQNKPLWQCYLGRFNDIHVPIRLE
                                PDLAKDLTEYLKVRSHDPEEAIRHDVIVSIV
                                HLLNFVVGERTLDKRWRVRKEAMMGLAQIYKK
                                KQIAWIKDKLLHIYYQNSIDDRLLVERIFAQ
                                MKCLYYLYATLDLNAVKALNEMWKCQNLLRH
                                KTDASVKAFISKVMVITRSLPDPGKAQDFMK
                                RKQLEVLVSPTCSCCKQAEGCVREITKKLGNP
                                FLLERIAPVHIDTESISALIKQVNKSIDGTAI
                                IRAGLELLKVLSFTHPISFHSAETFESLLACI
                                LQIFKNTGSKIEEDFPHIRSALLPVLHHKSKI
                                CIHAIFSSKEAQFAQIFEPLHKSLDPSNLEHI
                                LLAPDQFAAPLKSIVATFIVKDLLMNDRLPGI
                                VSPETMVKIQAIAKMMVRWLLGMKNHNSKSGT
                                DGDLTEQGGKISKPDMSRLRLAAGSAIVKLAQ
                                YQLCALAINDECYQVRQVFAQKLHKGLSRLRI
                                AKDPVKERRAHARQCLVKININVRREYLKQHA

```


YVVPYTIHLLAHPDYVKVQDIEQLKDVKECI
 ENNSHAFIRKMVENIKQTKDAQGPDDAKMNEI
 IMSKSTTYSLESPKDPVLPARFFTQPDKNFSI
 FFTPGKPKTTNVLGAVNKLSSAGKQSQTKEI
 SNPSSPGRIKGRLDSSMDHSENYDTMSSPI
 DLVRSELEKPRGRKKTPTVTEREEKLGMDDLTI
 RSRKRGHHTASEDEQQWPPEEKRLKEDIENEI
 GRPPKPLGGGTPKEPTMKTSKKGSKKSGPI
 SGNTEQKSKSKQHRVSRRAQQRAESSAII
 RPSKTPSPSQPKNV"

Differences in FEATURE.exon:

 New feature exon 174..377
 /gene = "AS3"
 /number = "3"

Differences in FEATURE.exon:

 New feature exon 378..464
 /gene = "AS3"
 /number = "4"

Differences in FEATURE.exon:

 New feature exon 465..562
 /gene = "AS3"
 /number = "5"

Differences in FEATURE.exon:

 New feature exon 563..689
 /gene = "AS3"
 /number = "6"

Differences in FEATURE.exon:

 New feature exon 690..770
 /gene = "AS3"
 /number = "7"

Differences in FEATURE.exon:

 New feature exon 771..911
 /gene = "AS3"
 /number = "8"

Differences in FEATURE.exon:

 New feature exon 912..1027
 /gene = "AS3"
 /number = "9"

Differences in FEATURE.exon:

 New feature exon 1028..1122
 /gene = "AS3"
 /number = "10"

Differences in FEATURE.exon:

New feature exon 1123..1268
 /gene = "AS3"
 /number = "11"

Differences in FEATURE.exon:

New feature exon 1269..1420
 /gene = "AS3"
 /number = "12"

Differences in FEATURE.exon:

New feature exon 1421..1534
 /gene = "AS3"
 /number = "13"

Differences in FEATURE.exon:

New feature exon 1535..1616
 /gene = "AS3"
 /number = "14"

Differences in FEATURE.exon:

New feature exon 1617..1665
 /gene = "AS3"
 /number = "15"

Differences in FEATURE.exon:

New feature exon 1666..1805
 /gene = "AS3"
 /number = "16"

Differences in FEATURE.exon:

New feature exon 1806..1921
 /gene = "AS3"
 /number = "17"

Differences in FEATURE.exon:

New feature exon 1922..2027
 /gene = "AS3"
 /number = "18"

Differences in FEATURE.exon:

New feature exon 2028..2188
 /gene = "AS3"
 /number = "19"

Differences in FEATURE.exon:

New feature exon 2189..2312
 /gene = "AS3"
 /number = "20"

Differences in FEATURE.exon:

New feature exon 2313..2471
 /gene = "AS3"
 /number = "21"

Differences in FEATURE.exon:

New feature exon 2472..2540
 /gene = "AS3"
 /number = "22"

Differences in FEATURE.exon:

New feature exon 2541..2677
 /gene = "AS3"
 /number = "23"

Differences in FEATURE.exon:

New feature exon 2678..2801
 /gene = "AS3"
 /number = "24"

Differences in FEATURE.exon:

New feature exon 2802..3006
 /gene = "AS3"
 /number = "25"

Differences in FEATURE.exon:

New feature exon 3007..3121
 /gene = "AS3"
 /number = "26"

Differences in FEATURE.exon:

New feature exon 3122..3254
 /gene = "AS3"
 /number = "27"

Differences in FEATURE.exon:

New feature exon 3255..3374
 /gene = "AS3"
 /number = "28"

Differences in FEATURE.exon:

New feature exon 3375..3437
 /gene = "AS3"
 /number = "29"

Differences in FEATURE.exon:

New feature exon 3438..3583
 /gene = "AS3"
 /number = "30"

Differences in FEATURE.exon:

```

-----
New feature      exon      3584..3689
                  /gene          = "AS3"
                  /number       = "31"

```

Differences in FEATURE.exon:

```

-----
New feature      exon      3690..4129
                  /gene          = "AS3"
                  /number       = "32"

```

Differences in FEATURE.exon:

```

-----
New feature      exon      4130..4354
                  /gene          = "AS3"
                  /number       = "33"

```

Differences in FEATURE.exon:

```

-----
New feature      exon      4355..4810
                  /gene          = "AS3"
                  /number       = "34"

```

Differences in REFERENCE:

Old reference:

```

      refline:      "2 (bases 1 to 4392)"
      authors:      "Geck,P., Szelei,J., Jimenez,J., Sonnenschein,
                    Soto,A.M."
      title:         "Early gene expression during androgen-induced
                    inhibition of proliferation of prostate cancer
                    cells: a new suppressor candidate on chromosome 17q
                    in the BRCA2-Rb1 locus"
      journal:       "J. Steroid Biochem. Mol. Biol. 68, 41-45"

```

New reference:

```

      refline:      "2 (bases 1 to 5253)"
      authors:      "Geck,P., Szelei,J., Jimenez,J., Sonnenschein,
                    Soto,A.M."
      title:         "Early gene expression during androgen-induced
                    inhibition of proliferation of prostate cancer
                    cells: a new suppressor candidate on chromosome 17q
                    in the BRCA2-Rb1 locus"
      journal:       "J. Steroid Biochem. Mol. Biol. 68 (1-2), 41-45"
      muid:          "99229875"
      pmid:          "10215036"

```

New reference:

```

      refline:      "4 (bases 1 to 5253)"
      authors:      "Geck,P., Szelei,J., Jimenez,J., Sonnenschein,
                    Soto,A.M."
      title:         "Direct Submission"
      journal:       "Submitted (05-APR-1999) Anatomy and Cell Biology
                    Tufts University Medical School, 136 Harrison
                    Avenue, Boston, MA 02111, USA"
      remark:        "Sequence update by submitter"

```

Differences in ORGANISM:

Changed lineage =

```

      old: "Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
            Mammalia; Eutheria; Primates; Catarrhini; Hominoidea;"

```

^
Homo."
new: "Eukaryota; Metazoa; Chordata; Craniata; Verte
Euteleostomi; Mammalia; Eutheria; Primates; C
^
Hominidae; Homo."

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[NCBI](#) | [NLM](#) | [NIH](#)



Sequence Revision History

PubMed

Nucleotide

Protein

Genome

Structure

PMC

Taxonomy

OMIM

Find (Accessions, GI numbers or Fasta style SeqIds) 

About Entrez

Show difference in format

	Gi	Version	Update Date
Entrez	4559409	2	Apr 5 1999 1:29
Search for Genes	4539617	1	Mar 30 1999 12:03

Search for Genes

LocusLink provides curated information for human, fruit fly, mouse, rat, and zebrafish

Query= gi|4559409|gb|U95825.2|HSU95825 Human androgen-induced prostatic proliferative shutoff associated protein (AS3) mRNA, complete cds (5253 letters)

Help/FAQ

<gi|4539617|gb|U95825.1|HSU95825 Human androgen-induced prostate proliferative shutoff associated protein (AS3) mRNA, complete cds
Length = 4392

Batch Entrez: Upload a file of GI or accession numbers to retrieve proteins or nucleotide sequences

Score = 7583 bits (3825), Expect = 0.0
Identities = 3959/4017 (98%)
Strand = Plus / Plus

Check sequence revision history

Query: 419 ggatacaaaagagccacagttcaataggtatTTTTTTTgcttgagaacattgct
Sbjct: 1 ggatacaaaagagccacaaattcaataggtatTTTTTTTtacttgagaacattgct

How to create WWW links to Entrez

Query: 479 caagtcataataacatatgctttgagttagaagatagcaatgaaattttcacccag
Sbjct: 61 caagtcataataacatatgctttgagttagaagatagcaatgaaattttcacccag

LinkOut

Cubby

Query: 539 cagaaccttattttcagttataaacaatggccacaatcagaaagtcctatgca
Sbjct: 121 cagaaccttattttcagttataaacaatggccacaatcagaaagtcctatgca

Related resources

BLAST

Query: 599 agaccttatgagctctattattttgtgaaggtgatacagtgctcaggagctttt
Sbjct: 181 agaccttatgagctctattattttgtgaaggtgatacagtgctcaggagctttt

Reference sequence project

LocusLink

Query: 659 ggTTTTtagtaaatctggtacctgctcataagaatttaaacagcaagcatatgat
Sbjct: 241 ggTTTTtagtaaatctggtacctgctcataagaatttaaacagcaagcatatgat

Clusters of orthologous groups

Protein reviews on the web

Query: 719 aaaggctttactgaagaggacagctcaagctattgagccatatattaccaannr
Sbjct: 301 aaaggctttactgaagaggacagctcaagctattgagccatatattaccactttt

Query: 779 tcaggttctgatgcttgggaaaacatctatcagcgatttgcagagcatgtctct

```
|||||
Sbjct: 361 tcaggttctgatgcttgggaaaacatctatcagcgatttgtcagagcatgtcttt

Query: 839 aattttggagctctacaatattgatagtcatttgctgctctctgttttacccca
|||||
Sbjct: 421 aattttggagctctacaatattgatagtcatttgctgctctctgttttacccca

Query: 899 atttaaattaaagagcaatgataatgaggagcgcctacaagttgttaaactact
|||||
Sbjct: 481 atttaaattaaagagcaatgataatgaggagcgcctacaagttgttaaactact

Query: 959 aatgtttggggcaaaggattcagaattggcttctcaaaacaagccactttggca
|||||
Sbjct: 541 aatgtttggggcaaaggattcagaattggcttctcaaaacaagccactttggca

Query: 1019 cttgggcaggtttaatgatatccatgtaccaatccgcctggaatgtgtgaaatt
|||||
Sbjct: 601 cttgggcaggtttaatgatatccatgtaccaatccgcctggaatgtgtgaaatt

Query: 1079 ccattgtctcatgaaccatcctgatttagcaaaagacttaacagagtatcttaa
|||||
Sbjct: 661 ccattgtctcatgaaccatcctgatttagcaaaagacttaacagagtatcttaa

Query: 1139 gtcacatgaccctgaggaagctattagacatgatgttattgtgtcaatagttac
|||||
Sbjct: 721 gtcacatgaccctgaggaagctattagacatgatgttattgtgtcaatagttac

Query: 1199 taaaaaggatattcttctgggtcaatgatcacttacttaattttgtgggagagag
|||||
Sbjct: 781 taaaaaggatattcttctgggtcaatgatcacttacttaattttgtgagagagag

Query: 1259 agacaaacgatggagagtacgcaaagaagccatgatgggacttgcccaaatttat
|||||
Sbjct: 841 agacaaacgatggagagtacgcaaagaagccatgatgggacttgcccaaatttat

Query: 1319 atatgctttacagtcagcagctggaaaagatgctgcaaaacagatagcatggat
|||||
Sbjct: 901 atatgctttacagtcagcagctggaaaagatgctgcaaaacagatagcatggat

Query: 1379 caaattgctacatatatattatcaaaatagtattgatgatcgactacttggtgaa
|||||
Sbjct: 961 caaattgctacatatatattatcaaaatagtattgatgatcgactacttggtgaa

Query: 1439 ctttgctcaatacatgggttcctcacaatttagaaactacagaacggatgaaatg
|||||
Sbjct: 1021 ctttgctcaatacatgggttcctcacaatttagaaactacagaacggatgaaatg

Query: 1499 ttacttgtagccacactggatttaaagtctgtgaaagcattgaatgaaatgtg
```

Sbjct: 1081 ttacttgtagccacactggatttaaagctgtgaaagcattgaatgaaatgtg

Query: 1559 tcaaaatctgctccgacatcaagtaaaggatttgcttgacttgattaagcaacc

Sbjct: 1141 tcaaaatctgctccgacatcaagtaaaggatttgcttgacttgattaagcaacc

Query: 1619 agatgccagtgtcaaggccatattttcaaaagtgatggttattacaagaagttt

Sbjct: 1201 agatgccagtgtcaaggccatattttcaaaagtgatggttattacaagaattt

Query: 1679 tcctggtaaggctcaggatttcatgaagaaattcacacagggtgttagaagatgat

Sbjct: 1261 tcctggtaaggctcaggatttcatgaagaaattcacacagggtgttagaagatgat

Query: 1739 aataagaaagcagttagaagtacttgtagtccaacatgctcctgcaagcaggct

Sbjct: 1321 aataagaaagcagttagaagtacttgtagtccaacatgctcctgcaagcaggct

Query: 1799 ttgtgtgctgaaataactaagaagttgggcaaccccaaacagcctacaaatcct

Sbjct: 1381 ttgtgtgctgaaataactaagaagttgggcaaccccaaacagcctacaaatcct

Query: 1859 ggaaatgatcaagtttctcttgagaggatagcacctgtgcacatagataccga

Sbjct: 1441 ggaaatgatcaagtttctcttgagaggatagcacctgtgcacatagataccga

Query: 1919 cagtgtcttattaacaagtgaacaaatcaatagatggaacagcagatgatga

Sbjct: 1501 cagtgtcttattaacaagtgaacaaatcaatagatggaacagcagatgatga

Query: 1979 ggggtgtccaactgatcaagccatcagagcaggctctgaactgcttaaggctact

Sbjct: 1561 ggggtgtccaactgatcaagccatcagagcaggctctgaactgcttaaggctact

Query: 2039 tacacatcccatctcatttcattctgctgaaacatttgatcattactggcctgt

Sbjct: 1621 tacacatcccatctcatttcattctgctgaaacatttgatcattactggcctgt

Query: 2099 aatggatgatgaaaaagtagcagaagctgcactacaaattttcaaaaacacagg

Sbjct: 1681 aatggatgatgaaaaagtagcagaagctgcactacaaattttcaaaaacacagg

Query: 2159 aattgaagaggattttccacacatcagatcagccttgcttctgttttacatca

Sbjct: 1741 aattgaagaggattttccacacatcagatcagccttgcttctgttttacatca

Query: 2219 taaaaaaggannnnnnngtcaagccaaatatgccattcattgtatccatgcgat

Sbjct: 1801 taaaaaaggacccccccgtcaagccaaatatgccattcattgtatccatgcgata
Query: 2279 tagtaaagaggcccagtttgacagatatattgagcctctgcataagagcctagat
Sbjct: 1861 tagtaaagagaccagtttgacagatatattgagcctctgcataagagcctagat
Query: 2339 caacctggaacatctcataacaccattgggttactattgggtcatattgctctcctt
Sbjct: 1921 caacctggaacatctcataacaccattgggttactattgggtcatattgctctcctt
Query: 2399 tgatcaatttgctgctcctttgaaatctttggtagctactttcattgtgaaagat
Sbjct: 1981 tgatcaatttgctgctcctttgaaatctttggtagctactttcattgtgaaagat
Query: 2459 catgaatgatcggcttccagggaaaaagacaactaaactttgggttccagatgaa
Sbjct: 2041 catgaatgatcggcttccagggaaaaagacaactaaactttgggttccagatgaa
Query: 2519 atctcctgagacaatgggtcaaaattcaggctattaaaatgatgggttcgatggcta
Sbjct: 2101 atctcctgagacaatgggtcaaaattcaggctattaaaatgatgggttcgatggcta
Query: 2579 aatgaaaaataatcacagtaaatacaggaacttctaccttaagattgctaacaaca
Sbjct: 2161 aatgaaaaataatcacagtaaatacaggaacttctaccttaagattgctaacaaca
Query: 2639 gcatagtgatggagacttgacagaacaggggaaaattagtaaaccagatatgtca
Sbjct: 2221 gcatagtgatggagacttgacagaacaggggaaaattagtaaaccagatatgtca
Query: 2699 gagacttgctgctgggagtgctattgtgaagctggcacaagaaccctgttaccat
Sbjct: 2281 gagacttgctgctgggagtgctattgtgaagctggcacaagaaccctgttaccat
Query: 2759 catcacattagaacaatatcagctatgtgcattagctatcaacgatgaatgctat
Sbjct: 2341 catcacattagaacaatatcagctatgtgcattagctatcaacgatgaatgctat
Query: 2819 aagacaagtgtttgccagaaacttcacaaaggcctttcccgtttacggcttcca
Sbjct: 2401 aagacaagtgtttgccagaaacttcacaaaggcctttcccgtttacggcttcca
Query: 2879 gtatatggcaatctgtgccctttgtgcaaaagatcctgtaaaggagagaagagct
Sbjct: 2461 gtatatggcaatctgtgccctttgtgcaaaagatcctgtaaaggagagaagagct
Query: 2939 taggcaatgtttggtgaaaaatataaatgtaaggcgggagtatctgaagcagcat

Sbjct: 2521 taggcaatgtttggtgaaaaatataaatgtaaggcgggagtatctgaagcagcat
Query: 2999 tgtagtgaaaaattattgtctcttctaccagagtatgttggtccatatacaatt
Sbjct: 2581 tgtagtgaaaaattattgtctcttctaccagagtatgttggtccatatacaatt
Query: 3059 tttggcacatgaccagattatgtcaaagtacaggatattgaacaacttaagat
Sbjct: 2641 tttggcacatgaccagattatgtcaaagtacaggatattgaacaacttaagat
Query: 3119 agaatgtctttggtttgttctggaaatattaatggctaaaaatgaaaataacagt
Sbjct: 2701 agaatgtctttggtttgttctggaaatattaatggctaaaaatgaaaataacagt
Query: 3179 ttttatcagaaagatggtagaaaatattaagcaaacaaaagatgcccaaggacca
Sbjct: 2761 ttttatcagaaagatggtagaaaatattaagcaaacaaaagatgcccaaggacca
Query: 3239 tgcaaaaatgaatgaaaaactgtacactgtgtgtgatgttgccatgaatatcatc
Sbjct: 2821 tgcaaaaatgaatgaaaaactgtacactgtgtgtgatgttgccatgaatatcatc
Query: 3299 aaagagtactacatacagtttggaatctcctaagacccgggtactaccagctcgt
Sbjct: 2881 aaagagtactacatacagtttggaatctcctaagacccgggtactaccagctcgt
Query: 3359 cactcaacctgacaagaatttcagtaacacccaaaaattatctgcctcctggaatc
Sbjct: 2941 cactcaacctgacaagaatttcagtaacacccaaaaattatctgcctcctggaatc
Query: 3419 atttttcactcctggaaaacctaacaaccaatgttctaggagctgttaacaac
Sbjct: 3001 atttttcactcctggaaaacctaacaaccaatgttctaggagctgttaacaac
Query: 3479 ttcatacagcaggcaagcaatctcagaccaaatacatcacgaatggaaactgtaggc
Sbjct: 3061 ttcatacagcaggcaagcaatctcagaccaaatacatcacgaatggaaactgtaggc
Query: 3539 aagcagcagctcaaatccaagctctcctggaagaataaaggggaggcttgatagt
Sbjct: 3121 aagcagcagctcaaatccaagctctcctggaagaataaaggggaggcttgatagt
Query: 3599 aatggatcacagtgaaaatgaagattacacaatgtcttcacctttgccggggaa
Sbjct: 3181 aatggatcacagtgaaaatgaagattacacaatgtcttcacctttgccggggaa
Query: 3659 tgacaagagagacgactctgatcttgtaagggtctgaattggagaagcctagaggc

Sbjct: 3241 |||
tgacaagagagacgactctgatcttgtaaggtctgaattggagaagcctagaggc

Query: 3719 nnnnncgcccgtcacagaacgggaggagaaattaggtatggatgacttgactaa
|||
Sbjct: 3301 aaaaacgcccgtcacagaacaggaggagaaattaggtatggatgacttgactaa

Query: 3779 acaggaacagagacctaagggcagtcagcgaagtcggaaaagaggccatacggct
|||
Sbjct: 3361 acaggaacagaaacctaagggcagtcagcgaagtcggaaaagaggccatacggct

Query: 3839 atctgatgaacagcagtggtcctgaggaaaagaggctcaaagaagatatattaga
|||
Sbjct: 3421 atctgatgaacagcagtggtcctgaggaaaagaggctcaaagaagatatattaga

Query: 3899 agatgaacagaatagtcgcgcaaaaaagggtaaaagaggccgaccaccaaaccct
|||
Sbjct: 3481 agatgaacagaatagtcgcgcaaaaaagggtaaaagaggccgaccaccaaaccct

Query: 3959 tggagggtacaccaaagaagagccaacaatgaaaacttctaaaaaggaagcnnr
|||
Sbjct: 3541 tggagggtacaccaaagaagagccaacaatgaaaacttctaaaaaggaagcaa

Query: 4019 ntctggacctccagcaccagaggaggaggaagaagaagaaagacaaagtggaaat
|||
Sbjct: 3601 atctggacctccagcaccagaggaggaggaagaagaagaaagacaaagtggaaat

Query: 4079 acagaagtcctaaaagcaaacagcaccgagtggtcaaggagagcacagcagagagca
|||
Sbjct: 3661 acagaagtcctaaaagcaaacagcaccgagtggtcaaggagagcacagcagagagca

Query: 4139 ttctgaatctagtgaattgaatccacacagtcacaccacagaaaggacgagg
|||
Sbjct: 3721 tcctgaatctagtgaattgaatccacacagtcacaccacagaaaggacgagg

Query: 4199 atcaaaaacgccatcaccatcacaaccnnnnnnntgtgtaagttgtaaattat
|||
Sbjct: 3781 atcaaaaacgccatcaccatcacaaccnaaaatgtgtaagttgtaaattat

Query: 4259 tcaaaccaatttcaaattattttgcaaaaagttcctaaatttgtaaacatacatat
|||
Sbjct: 3841 tcaaaccaatttcaaattattttgcaaaaagttcctaaatttgtaaacatacatat

Query: 4319 tatttaaatccatatatttagccccattacactaggtacggcggcgaagtgtc
|||
Sbjct: 3901 tatttaaatccatatatttagccccattacactaggtacggcggcgaagtgtc

Query: 4379 gaacggcgatgaacaaatgtaattaataactttctctgtgaaagctttggaaa

|||||
Sbjct: 3961 gaacggcgatgaacaaatgtaattaataactttctctgtgaaagctttggaaaaa

Score = 396 bits (200), Expect = e-113
Identities = 200/200 (100%)
Strand = Plus / Plus

Query: 4458 ggtcaagcttgaggctgaataaagcctttgatgcacaaaatgggactgctgaaga
|||||
Sbjct: 4040 ggtcaagcttgaggctgaataaagcctttgatgcacaaaatgggactgctgaaga

Query: 4518 cagttggaccttactttggtgaccccatatcatttgggtcacatgcttttagccat
|||||
Sbjct: 4100 cagttggaccttactttggtgaccccatatcatttgggtcacatgcttttagccat

Query: 4578 tggtaacattgactatggagtcttgtgaaagtgtaatgtgcgatggctatgtaga
|||||
Sbjct: 4160 tggtaacattgactatggagtcttgtgaaagtgtaatgtgcgatggctatgtaga

Query: 4638 agaagaaacttgtaaataatc 4657
|||||
Sbjct: 4220 agaagaaacttgtaaataatc 4239

Score = 274 bits (138), Expect = 7e-76
Identities = 138/138 (100%)
Strand = Plus / Plus

Query: 4673 aatgtttctgatttctgaagtgcttgtatagcttttatctgcggctttaaactga
|||||
Sbjct: 4255 aatgtttctgatttctgaagtgcttgtatagcttttatctgcggctttaaactga

Query: 4733 cccgactgtttattggatctattgatttgaaaagaatttggttaggatagatctta
|||||
Sbjct: 4315 cccgactgtttattggatctattgatttgaaaagaatttggttaggatagatctta

Query: 4793 taatctgtcagtgtttgt 4810
|||||
Sbjct: 4375 taatctgtcagtgtttgt 4392

Score = 26.3 bits (13), Expect = 0.28
Identities = 13/13 (100%)
Strand = Plus / Minus

Query: 1943 caaatcaatagat 1955
|||||
Sbjct: 4343 caaatcaatagat 4331

Score = 26.3 bits (13), Expect = 0.28
Identities = 13/13 (100%)
Strand = Plus / Minus

Query: 4749 atctattgatttg 4761
 |||||
Sbjct: 1537 atctattgatttg 1525

Score = 22.3 bits (11), Expect = 4.4
Identities = 11/11 (100%)
Strand = Plus / Minus

Query: 718 caaaggcttta 728
 |||||
Sbjct: 4069 caaaggcttta 4059

Score = 22.3 bits (11), Expect = 4.4
Identities = 11/11 (100%)
Strand = Plus / Minus

Query: 2384 tgctctccttg 2394
 |||||
Sbjct: 3703 tgctctccttg 3693

Score = 22.3 bits (11), Expect = 4.4
Identities = 11/11 (100%)
Strand = Plus / Plus

Query: 5118 aagaagaaaga 5128
 |||||
Sbjct: 3633 aagaagaaaga 3643

Score = 22.3 bits (11), Expect = 4.4
Identities = 11/11 (100%)
Strand = Plus / Minus

Query: 2307 tttgagcctct 2317
 |||||
Sbjct: 3460 tttgagcctct 3450

Score = 22.3 bits (11), Expect = 4.4
Identities = 11/11 (100%)

Strand = Plus / Minus

Query: 1079 ccattgtctca 1089
 |||||
Sbjct: 2117 ccattgtctca 2107

Score = 22.3 bits (11), Expect = 4.4
Identities = 11/11 (100%)
Strand = Plus / Minus

Query: 637 tgtctcaggag 647
 |||||
Sbjct: 2113 tgtctcaggag 2103

Score = 22.3 bits (11), Expect = 4.4
Identities = 11/11 (100%)
Strand = Plus / Minus

Query: 4111 caaggagagca 4121
 |||||
Sbjct: 1976 caaggagagca 1966

Score = 22.3 bits (11), Expect = 4.4
Identities = 11/11 (100%)
Strand = Plus / Minus

Query: 3868 agaggctcaaa 3878
 |||||
Sbjct: 1899 agaggctcaaa 1889

Score = 22.3 bits (11), Expect = 4.4
Identities = 11/11 (100%)
Strand = Plus / Minus

Query: 2148 acaggaagcaa 2158
 |||||
Sbjct: 1785 acaggaagcaa 1775

Score = 22.3 bits (11), Expect = 4.4
Identities = 11/11 (100%)
Strand = Plus / Minus

Query: 2193 ttgcttctgt 2203
 |||||

Sbjct: 1740 ttgcttcctgt 1730

Score = 22.3 bits (11), Expect = 4.4
Identities = 11/11 (100%)
Strand = Plus / Plus

Query: 353 ttacacatccc 363
 |||||
Sbjct: 1620 ttacacatccc 1630

Score = 22.3 bits (11), Expect = 4.4
Identities = 11/11 (100%)
Strand = Plus / Minus

Query: 5069 tattgatttgt 5079
 |||||
Sbjct: 1534 tattgatttgt 1524

Score = 22.3 bits (11), Expect = 4.4
Identities = 11/11 (100%)
Strand = Plus / Minus

Query: 2525 tgagacaatgg 2535
 |||||
Sbjct: 671 tgagacaatgg 661

Score = 22.3 bits (11), Expect = 4.4
Identities = 11/11 (100%)
Strand = Plus / Minus

Query: 4477 taaagcctttg 4487
 |||||
Sbjct: 310 taaagcctttg 300

Score = 22.3 bits (11), Expect = 4.4
Identities = 11/11 (100%)
Strand = Plus / Minus

Query: 2521 ctcttgagaca 2531
 |||||
Sbjct: 229 ctcttgagaca 219

Lambda	K	H
1.37	0.711	1.31

Gapped
Lambda K H
1.37 0.711 1.31

Matrix: blastn matrix:1 -3
Gap Penalties: Existence: 5, Extension: 2
Number of Hits to DB: 38
Number of Sequences: 0
Number of extensions: 38
Number of successful extensions: 38
Number of sequences better than 10.0: 1
Number of HSP's better than 10.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 29
length of query: 5253
length of database: 4392
effective HSP length: 12
effective length of query: 5241
effective length of database: 4380
effective search space: 22955580
effective search space used: 22955580
T: 0
A: 0
X1: 6 (11.9 bits)
X2: 15 (29.7 bits)
S1: 12 (24.3 bits)
S2: 11 (22.3 bits)

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[NCBI](#) | [NLM](#) | [NIH](#)



Sequence Revision History

PubMed

Nucleotide

Protein

Genome

Structure

PMC

Taxonomy

OMIM

Find (Accessions, GI numbers or Fasta style SeqIds) 

About Entrez

Show difference in format

Entrez

Gi	Version	Update Date
4539617	1	Mar 30 1999 12:03
4559409	2	Apr 5 1999 1:29

Search for Genes

LocusLink provides curated information for human, fruit fly, mouse, rat, and zebrafish

Query= gi|4539617|gb|U95825.1|HSU95825 Human androgen-induced prost proliferative shutoff associated protein (AS3) mRNA, complete cds (4392 letters)

Help/FAQ

<gi|4559409|gb|U95825.2|HSU95825 Human androgen-induced prostate proliferative shutoff associated protein (AS3) mRNA, complete cds
Length = 5253

Batch Entrez: Upload a file of GI or accession numbers to retrieve proteins OR nucleotide sequences

Score = 7547 bits (3807), Expect = 0.0
Identities = 3953/4017 (98%)
Strand = Plus / Plus

Check sequence revision history

Query: 1 ggatacaaaagagcccacaaattcaataggtatTTTTATTtacttgagaacattgct
Sbjct: 419 ggatacaaaagagcccacagttcaataggtatTTTTATTtcttgagaacattgct

How to create WWW links to Entrez

Query: 61 caagtcataataacatatgctttgagttagaagatagcaatgaaatTTTcaccac
Sbjct: 479 caagtcataataacatatgctttgagttagaagatagcaatgaaatTTTcaccac

LinkOut

Cubby

Query: 121 cagaaccttattttcagttataaacaatggccacaatcagaaagtccatatgca
Sbjct: 539 cagaaccttattttcagttataaacaatggccacaatcagaaagtccatatgca

Related resources

BLAST

Query: 181 agaccttatgagctctattattttgtgaaggtgatacagtgctcaggagctttt
Sbjct: 599 agaccttatgagctctattattttgtgaaggtgatacagtgctcaggagctttt

Reference sequence project

LocusLink

Query: 241 ggTTTTagtaaactctggtacctgctcataagaatttaaacagcaagcatatgat
Sbjct: 659 ggTTTTagtaaactctggtacctgctcataagaatttaaacagcaagcatatgat

Clusters of orthologous groups

Protein reviews on the web

Query: 301 aaaggctttactgaagaggacagctcaagctattgagccatatattaccacnnr
Sbjct: 719 aaaggctttactgaagaggacagctcaagctattgagccatatattaccaattt

Query: 361 tcaggttctgatgcttgggaaaacatctatcagcgatttgtcagagcatgtctt

```
|||||
Sbjct: 779 tcaggttctgatgcttgggaaaacatctatcagcgatttgtcagagcatgtctct

Query: 421 aattttggagctctacaatattgatagtcatttgctgctctctgttttacccca
|||||
Sbjct: 839 aattttggagctctacaatattgatagtcatttgctgctctctgttttacccca

Query: 481 atttaaattaaagagcaatgataatgaggagcgcctacaagttgttaaactact
|||||
Sbjct: 899 atttaaattaaagagcaatgataatgaggagcgcctacaagttgttaaactact

Query: 541 aatgtttggggcaaaggattcagaattggcttctcaaaacaagccactttggca
|||||
Sbjct: 959 aatgtttggggcaaaggattcagaattggcttctcaaaacaagccactttggca

Query: 601 cttgggcaggtttaatgatatccatgtaccaatccgcctggaatgtgtgaaatt
|||||
Sbjct: 1019 cttgggcaggtttaatgatatccatgtaccaatccgcctggaatgtgtgaaatt

Query: 661 ccattgtctcatgaaccatcctgatttagcaaaagacttaacagagtatcttaa
|||||
Sbjct: 1079 ccattgtctcatgaaccatcctgatttagcaaaagacttaacagagtatcttaa

Query: 721 gtcacatgaccctgaggaagctattagacatgatgttattgtgtcaatagttac
|||||
Sbjct: 1139 gtcacatgaccctgaggaagctattagacatgatgttattgtgtcaatagttac

Query: 781 taaaaaggatattcttctggtcaatgatcacttacttaattttgtgagagagag
|||||
Sbjct: 1199 taaaaaggatattcttctggtcaatgatcacttacttaattttgtgggagagag

Query: 841 agacaaacgatggagagtagcgaagaagccatgatgggacttgcccaaatttat
|||||
Sbjct: 1259 agacaaacgatggagagtagcgaagaagccatgatgggacttgcccaaatttat

Query: 901 atatgctttacagtcagcagctggaaaagatgctgcaaaacagatagcatggat
|||||
Sbjct: 1319 atatgctttacagtcagcagctggaaaagatgctgcaaaacagatagcatggat

Query: 961 caaattgctacatatatattatcaaaatagattgatgatcgactacttggtgaa
|||||
Sbjct: 1379 caaattgctacatatatattatcaaaatagattgatgatcgactacttggtgaa

Query: 1021 ctttgctcaatacatgggttcctcacaatttagaaactacagaacggatgaaatg
|||||
Sbjct: 1439 ctttgctcaatacatgggttcctcacaatttagaaactacagaacggatgaaatg

Query: 1081 ttacttgtagccacactggatttaaagtgtgtgaaagcattgaatgaaatgtg
```

Sbjct: 1499 ttacttgtatgccacactggatttaaagctgtgaaagcattgaatgaaatgtg
Query: 1141 tcaaaatctgctccgacatcaagtaaaggatttgcttgacttgattaagcaacc
Sbjct: 1559 tcaaaatctgctccgacatcaagtaaaggatttgcttgacttgattaagcaacc
Query: 1201 agatgccagtgtcaaggccatattttcaaaagtgatggttattacaagaaattt
Sbjct: 1619 agatgccagtgtcaaggccatattttcaaaagtgatggttattacaagaagt
Query: 1261 tcctggtaaggctcaggatttcatgaagaaattcacacaggtgttagaatgat
Sbjct: 1679 tcctggtaaggctcaggatttcatgaagaaattcacacaggtgttagaatgat
Query: 1321 aataagaaagcagttagaagtacttgtagtccaacatgctcctgcaagcaggct
Sbjct: 1739 aataagaaagcagttagaagtacttgtagtccaacatgctcctgcaagcaggct
Query: 1381 ttgtgtgctgaaataactaagaagttgggcaaccccaacagcctacaaatcct
Sbjct: 1799 ttgtgtgctgaaataactaagaagttgggcaaccccaacagcctacaaatcct
Query: 1441 ggaaatgatcaagtttctcttgagaggatagcacctgtgcacatagataccga
Sbjct: 1859 ggaaatgatcaagtttctcttgagaggatagcacctgtgcacatagataccga
Query: 1501 cagtgtctttattaacaagtgaacaaatcaatagatggaacagcagatgatga
Sbjct: 1919 cagtgtctttattaacaagtgaacaaatcaatagatggaacagcagatgatga
Query: 1561 ggggtgttccaactgatcaagccatcagagcaggtcttgaactgcttaaggctact
Sbjct: 1979 ggggtgttccaactgatcaagccatcagagcaggtcttgaactgcttaaggctact
Query: 1621 tacacatcccatctcatttcattctgctgaaacatttgaatcattactggcttgt
Sbjct: 2039 tacacatcccatctcatttcattctgctgaaacatttgaatcattactggcttgt
Query: 1681 aatggatgatgaaaaagtagcagaagctgcactacaaattttcaaaaacacagg
Sbjct: 2099 aatggatgatgaaaaagtagcagaagctgcactacaaattttcaaaaacacagg
Query: 1741 aattgaagaggattttccacacatcagatcagccttgcttctgttttacatca
Sbjct: 2159 aattgaagaggattttccacacatcagatcagccttgcttctgttttacatca
Query: 1801 taaaaaaggannnnnnngtcaagccaaatatgccattcattgtatccatgcgat

Sbjct: 2219 taaaaaaggaccccccggtcaagccaaatatgccattcattgtatccatgcgata
Query: 1861 tagtaaagagaccagtttgacagatatattgagcctctgcataagagcctagat
Sbjct: 2279 tagtaaagaggcccagtttgacagatatattgagcctctgcataagagcctagat
Query: 1921 caacctggaacatctcataacaccattgggttactattgggtcatattgctctcctt
Sbjct: 2339 caacctggaacatctcataacaccattgggttactattgggtcatattgctctcctt
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Sbjct: 2399 tgatcaatttgctgctccttggaaatcttgggtagctactttcattgtgaaagat
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Sbjct: 2459 catgaatgatcggcttccagggaaaaagacaactaaactttgggttccagatga
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Sbjct: 2519 atctcctgagacaatgggtcaaaattcaggctattaaaatgatgggttcgatggcta
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Sbjct: 2579 aatgaaaaataatcacagtaaatcaggaacttctaccttaagattgctaacaaca
Query: 2221 gcatagtgatggagacttgacagaacaggggaaaattagtaaaccagatatgtca
Sbjct: 2639 gcatagtgatggagacttgacagaacaggggaaaattagtaaaccagatatgtca
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Sbjct: 2699 gagacttgctgctgggagtgctattgtgaagctggcacaagaaccctgttaccat
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Sbjct: 2759 catcacattagaacaatatcagctatgtgcattagctatcaacgatgaatgctat
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Sbjct: 2819 aagacaagtgtttgccagaaacttcacaaaggcctttcccgtttacggcttcca
Query: 2461 gtatatggcaatctgtgccctttgtgcaaaagatcctgtaaaggagagaagagct
Sbjct: 2879 gtatatggcaatctgtgccctttgtgcaaaagatcctgtaaaggagagaagagct
Query: 2521 taggcaatggttggtgaaaaatataaatgtaaggcgggagtatctgaagcagcat

Sbjct: 2939 taggcaatgtttggtgaaaaatataaatgtaaggcgggagtatctgaagcagcat
Query: 2581 tgttagtgaaaaattattgtctcttctaccagagtatggtgttccatatacaatt
Sbjct: 2999 tgttagtgaaaaattattgtctcttctaccagagtatggtgttccatatacaatt
Query: 2641 tttggcacatgaccagattatgtcaaagtacaggatattgaacaacttaagat
Sbjct: 3059 tttggcacatgaccagattatgtcaaagtacaggatattgaacaacttaagat
Query: 2701 agaatgtctttggtttgttctggaaatattaatggctaaaaatgaaaataacagt
Sbjct: 3119 agaatgtctttggtttgttctggaaatattaatggctaaaaatgaaaataacagt
Query: 2761 ttttatcagaaagatggtagaaaatattaacaacaaaagatgccaaggacc
Sbjct: 3179 ttttatcagaaagatggtagaaaatattaagcaacaaaagatgccaaggacc
Query: 2821 tgcaaaaatgaatgaaaaactgtacactgtgtgtgatgttgccatgaatatcatc
Sbjct: 3239 tgcaaaaatgaatgaaaaactgtacactgtgtgtgatgttgccatgaatatcatc
Query: 2881 aaagagtactacatacagtttggaatctcctaagaccgggtactaccagctcgt
Sbjct: 3299 aaagagtactacatacagtttggaatctcctaagaccgggtactaccagctcgt
Query: 2941 cactcaacctgacaagaatttcagtaacacccaaaaattatctgcctcctgaaatc
Sbjct: 3359 cactcaacctgacaagaatttcagtaacacccaaaaattatctgcctcctgaaatc
Query: 3001 atttttcactcctggaaaacctaaaacaaccaatgttctaggagctgttaacaac
Sbjct: 3419 atttttcactcctggaaaacctaaaacaaccaatgttctaggagctgttaacaac
Query: 3061 ttcatcagcaggcaagcaatctcagaccaaatacatcacgaatggaaactgtaagc
Sbjct: 3479 ttcatcagcaggcaagcaatctcagaccaaatacatcacgaatggaaactgtaggc
Query: 3121 aagcagcagctcaaatacaagctctcctggaagaataaagggaggcttgatagt
Sbjct: 3539 aagcagcagctcaaatacaagctctcctggaagaataaagggaggcttgatagt
Query: 3181 aatggatcacagtgaaaatgaagattacacaatgtcttcacctttgccggggnnr
Sbjct: 3599 aatggatcacagtgaaaatgaagattacacaatgtcttcacctttgccggggaa
Query: 3241 tgacaagagagacgactctgatcttgtaaggctctgaattggagaagcctagaggc

Sbjct: 3659 |||
tgacaagagagacgactctgatcttgtaaggctgaattggagaagcctagaggc

Query: 3301 nnnnncgcccgtcacagaacaggaggagaaattaggtatggatgacttgactaa
|||
Sbjct: 3719 aaaaacgcccgtcacagaacgggaggagaaattaggtatggatgacttgactaa

Query: 3361 acaggaacagaaacctaagggcagtcagcgaagtcggaaaagaggccatacggct
|||
Sbjct: 3779 acaggaacagagacctaagggcagtcagcgaagtcggaaaagaggccatacggct

Query: 3421 atctgatgaacagcagtgccctgaggaaaagaggctcaaagaagatatattaga
|||
Sbjct: 3839 atctgatgaacagcagtgccctgaggaaaagaggctcaaagaagatatattaga

Query: 3481 agatgaacagaatagtcgccaaaaaagggtaaaagaggccgaccacccaaaacct
|||
Sbjct: 3899 agatgaacagaatagtcgccaaaaaagggtaaaagaggccgaccacccaaaacct

Query: 3541 tggaggtagacccaaaagaagagccaacaatgaaaacttctaaaaaaggaagcnn
|||
Sbjct: 3959 tggaggtagacccaaaagaagagccaacaatgaaaacttctaaaaaaggaagcaa

Query: 3601 ntctggacctccagcaccagaggaggaggaagaagaagaaagacaaagtggaaat
|||
Sbjct: 4019 atctggacctccagcaccagaggaggaggaagaagaagaaagacaaagtggaaat

Query: 3661 acagaagtccaaaagcaaacagcaccgagtggtcaaggagagcacagcagagagc
|||
Sbjct: 4079 acagaagtccaaaagcaaacagcaccgagtggtcaaggagagcacagcagagagc

Query: 3721 tcctgaatctagtgcattgaatccacacagtcacacaccagaaaggacgagg
|||
Sbjct: 4139 tcctgaatctagtgcattgaatccacacagtcacacaccagaaaggacgagg

Query: 3781 atcaaaaacgccatcaccatcacaaccnnnnnnntgtgtaagttgtaaatatt
|||
Sbjct: 4199 atcaaaaacgccatcaccatcacaaccnaaaatgtgtaagttgtaaatatt

Query: 3841 tcaaaccaatttcaaattattttgcaaaagttcctaaatttgtaaacatacatat
|||
Sbjct: 4259 tcaaaccaatttcaaattattttgcaaaagttcctaaatttgtaaacatacatat

Query: 3901 tatttaaattccatatatttagccccattacactaggtacggcggcgaagtgtc
|||
Sbjct: 4319 tatttaaattccatatatttagccccattacactaggtacggcggcgaagtgtc

Query: 3961 gaacggcgatgaacaaatgtaattaataactttctctgtgaaagctttggaaaa

|||||
Sbjct: 4379 gaacggcgatgaacaaatgtaattaataactttctctgtgaaagctttggaaaaa

Score = 396 bits (200), Expect = e-113

Identities = 200/200 (100%)

Strand = Plus / Plus

Query: 4040 ggtcaagcttgaggctgaataaagcctttgatgcacaaaatgggactgctgaaga

|||||
Sbjct: 4458 ggtcaagcttgaggctgaataaagcctttgatgcacaaaatgggactgctgaaga

Query: 4100 cagttggaccttactttggtgaccccatatcatttgggtcacatgcttttagccat

|||||
Sbjct: 4518 cagttggaccttactttggtgaccccatatcatttgggtcacatgcttttagccat

Query: 4160 tggtaacattgactatggagtcttgtgaaagtgtaatgtgcatggctatgtaga

|||||
Sbjct: 4578 tggtaacattgactatggagtcttgtgaaagtgtaatgtgcatggctatgtaga

Query: 4220 agaagaaacttgtaaataatc 4239

|||||
Sbjct: 4638 agaagaaacttgtaaataatc 4657

Score = 274 bits (138), Expect = 7e-76

Identities = 138/138 (100%)

Strand = Plus / Plus

Query: 4255 aatgtttctgatttctgaagtgcttgtatagcttttatctgaggctttaactga

|||||
Sbjct: 4673 aatgtttctgatttctgaagtgcttgtatagcttttatctgaggctttaactga

Query: 4315 cccgactgtttattggatctattgatttgaaaagaatttgtaggatagatctta

|||||
Sbjct: 4733 cccgactgtttattggatctattgatttgaaaagaatttgtaggatagatctta

Query: 4375 taatctgtcagtgtttgt 4392

|||||
Sbjct: 4793 taatctgtcagtgtttgt 4810

Score = 26.3 bits (13), Expect = 0.28

Identities = 13/13 (100%)

Strand = Plus / Minus

Query: 1525 caaatcaatagat 1537

|||||
Sbjct: 4761 caaatcaatagat 4749

Score = 26.3 bits (13), Expect = 0.28
Identities = 13/13 (100%)
Strand = Plus / Minus

Query: 4331 atctattgatttg 4343
 |||||||
Sbjct: 1955 atctattgatttg 1943

Score = 22.3 bits (11), Expect = 4.4
Identities = 11/11 (100%)
Strand = Plus / Plus

Query: 3633 aagaagaaaga 3643
 |||||||
Sbjct: 5118 aagaagaaaga 5128

Score = 22.3 bits (11), Expect = 4.4
Identities = 11/11 (100%)
Strand = Plus / Minus

Query: 1524 acaaatcaata 1534
 |||||||
Sbjct: 5079 acaaatcaata 5069

Score = 22.3 bits (11), Expect = 4.4
Identities = 11/11 (100%)
Strand = Plus / Minus

Query: 300 caaaggcttta 310
 |||||||
Sbjct: 4487 caaaggcttta 4477

Score = 22.3 bits (11), Expect = 4.4
Identities = 11/11 (100%)
Strand = Plus / Minus

Query: 1966 tgctctccttg 1976
 |||||||
Sbjct: 4121 tgctctccttg 4111

Score = 22.3 bits (11), Expect = 4.4
Identities = 11/11 (100%)

Strand = Plus / Minus

Query: 1889 tttgagcctct 1899
 |||||
Sbjct: 3878 tttgagcctct 3868

Score = 22.3 bits (11), Expect = 4.4
Identities = 11/11 (100%)
Strand = Plus / Minus

Query: 661 ccattgtctca 671
 |||||
Sbjct: 2535 ccattgtctca 2525

Score = 22.3 bits (11), Expect = 4.4
Identities = 11/11 (100%)
Strand = Plus / Minus

Query: 219 tgtctcaggag 229
 |||||
Sbjct: 2531 tgtctcaggag 2521

Score = 22.3 bits (11), Expect = 4.4
Identities = 11/11 (100%)
Strand = Plus / Minus

Query: 3693 caaggagagca 3703
 |||||
Sbjct: 2394 caaggagagca 2384

Score = 22.3 bits (11), Expect = 4.4
Identities = 11/11 (100%)
Strand = Plus / Minus

Query: 3450 agaggctcaaa 3460
 |||||
Sbjct: 2317 agaggctcaaa 2307

Score = 22.3 bits (11), Expect = 4.4
Identities = 11/11 (100%)
Strand = Plus / Minus

Query: 1730 acaggaagcaa 1740
 |||||

Sbjct: 2203 acaggaagcaa 2193

Score = 22.3 bits (11), Expect = 4.4
Identities = 11/11 (100%)
Strand = Plus / Minus

Query: 1775 ttgcttcctgt 1785

|||||

Sbjct: 2158 ttgcttcctgt 2148

Score = 22.3 bits (11), Expect = 4.4
Identities = 11/11 (100%)
Strand = Plus / Minus

Query: 2107 tgagacaatgg 2117

|||||

Sbjct: 1089 tgagacaatgg 1079

Score = 22.3 bits (11), Expect = 4.4
Identities = 11/11 (100%)
Strand = Plus / Minus

Query: 4059 taaagcctttg 4069

|||||

Sbjct: 728 taaagcctttg 718

Score = 22.3 bits (11), Expect = 4.4
Identities = 11/11 (100%)
Strand = Plus / Minus

Query: 2103 ctcctgagaca 2113

|||||

Sbjct: 647 ctcctgagaca 637

Score = 22.3 bits (11), Expect = 4.4
Identities = 11/11 (100%)
Strand = Plus / Plus

Query: 1620 ttacacatccc 1630

|||||

Sbjct: 353 ttacacatccc 363

Lambda	K	H
1.37	0.711	1.31

Gapped

Lambda	K	H
1.37	0.711	1.31

Matrix: blastn matrix:1 -3
Gap Penalties: Existence: 5, Extension: 2
Number of Hits to DB: 39
Number of Sequences: 0
Number of extensions: 39
Number of successful extensions: 39
Number of sequences better than 10.0: 1
Number of HSP's better than 10.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 29
length of query: 4392
length of database: 5253
effective HSP length: 12
effective length of query: 4380
effective length of database: 5241
effective search space: 22955580
effective search space used: 22955580
T: 0
A: 0
X1: 6 (11.9 bits)
X2: 15 (29.7 bits)
S1: 12 (24.3 bits)
S2: 11 (22.3 bits)

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